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1600

RAW SEQUENCE LISTING

DATE: 09/11/2003

PATENT APPLICATION: US/09/830,502A

TIME: 10:33:46

Input Set : A:\C26151.app

Output Set : N:\CRF4\09112003\I830502A.raw

3 <110> APPLICANT: Barany, Francis
 4 Cao, Weiguo
 5 Tong, Jie
 7 <120> TITLE OF INVENTION: HIGH FIDELITY THERMOSTABLE LIGASE AND USES THEREOF
 9 <130> FILE REFERENCE: 19603/2615
 11 <140> CURRENT APPLICATION NUMBER: 09/830,502A
 12 <141> CURRENT FILING DATE: 1999-10-29
 14 <150> PRIOR APPLICATION NUMBER: 60/106,461
 15 <151> PRIOR FILING DATE: 1998-10-30
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/25437
 18 <151> PRIOR FILING DATE: 1999-10-29
 20 <160> NUMBER OF SEQ ID NOS: 20
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 674
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Thermus sp.
 29 <400> SEQUENCE: 1
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 31 1 5 10 15
 33 Ile Arg Tyr His Asn Tyr Leu Tyr Tyr Val Leu Asp Ala Pro Glu Ile
 34 20 25 30
 36 Ser Asp Ala Glu Tyr Asp Arg Leu Leu Arg Glu Leu Lys Glu Leu Glu
 37 35 40 45
 39 Glu Arg Phe Pro Glu Leu Lys Ser Pro Asp Ser Pro Thr Glu Gln Val
 40 50 55 60
 42 Gly Ala Arg Pro Leu Glu Ala Thr Phe Arg Pro Val Arg His Pro Thr
 43 65 70 75 80
 45 Arg Met Tyr Ser Leu Asp Asn Ala Phe Ser Leu Asp Glu Val Arg Ala
 46 85 90 95
 48 Phe Glu Glu Arg Ile Glu Arg Ala Leu Gly Arg Lys Gly Pro Phe Leu
 49 100 105 110
 51 Tyr Thr Val Glu Arg Lys Val Asp Gly Leu Ser Val Asn Leu Tyr Tyr
 52 115 120 125
 54 Glu Glu Gly Ile Leu Val Phe Gly Ala Thr Arg Gly Asp Gly Glu Thr
 55 130 135 140
 57 Gly Glu Glu Val Thr Gln Asn Leu Leu Thr Ile Pro Thr Ile Pro Arg
 58 145 150 155 160
 60 Arg Leu Thr Gly Val Pro Asp Arg Leu Glu Val Arg Gly Glu Val Tyr
 61 165 170 175
 63 Met Pro Ile Glu Ala Phe Leu Arg Leu Asn Gln Glu Leu Glu Glu Ala
 64 180 185 190
 66 Gly Glu Arg Ile Phe Lys Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu

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67          195          200          205
69 Arg Gln Lys Asp Pro Arg Val Thr Ala Arg Arg Gly Leu Arg Ala Thr
70          210          215          220
72 Phe Tyr Ala Leu Gly Leu Gly Leu Glu Glu Thr Gly Leu Lys Ser Gln
73 225          230          235          240
75 His Asp Leu Leu Leu Trp Leu Arg Glu Arg Gly Phe Pro Val Glu His
76          245          250          255
78 Gly Phe Thr Arg Ala Leu Gly Ala Glu Gly Val Glu Glu Val Tyr Gln
79          260          265          270
81 Ala Trp Leu Lys Glu Arg Arg Lys Leu Pro Phe Glu Ala Asp Gly Val
82          275          280          285
84 Val Val Lys Leu Asp Asp Leu Ala Leu Trp Arg Glu Leu Gly Tyr Thr
85          290          295          300
87 Ala Arg Thr Pro Arg Phe Ala Leu Ala Tyr Lys Phe Pro Ala Glu Glu
88 305          310          315          320
90 Lys Glu Thr Arg Leu Leu Ser Val Ala Phe Gln Val Gly Arg Thr Gly
91          325          330          335
93 Arg Ile Thr Pro Val Gly Val Leu Glu Pro Val Phe Ile Glu Gly Ser
94          340          345          350
96 Glu Val Ser Arg Val Thr Leu His Asn Glu Ser Phe Ile Glu Glu Leu
97          355          360          365
99 Asp Val Arg Ile Gly Asp Trp Val Leu Val His Lys Ala Gly Gly Val
100          370          375          380
102 Ile Pro Glu Val Leu Arg Val Leu Lys Glu Arg Arg Thr Gly Glu Glu
103 385          390          395          400
105 Lys Pro Ile Ile Trp Pro Glu Asn Cys Pro Glu Cys Gly His Ala Leu
106          405          410          415
108 Ile Lys Glu Gly Lys Val His Arg Cys Pro Asn Pro Leu Cys Pro Ala
109          420          425          430
111 Lys Arg Phe Glu Ala Ile Arg His Tyr Ala Ser Arg Lys Ala Met Asp
112          435          440          445
114 Ile Gln Gly Leu Gly Glu Lys Leu Ile Glu Lys Leu Leu Glu Lys Gly
115          450          455          460
117 Leu Val Arg Asp Val Ala Asp Leu Tyr Arg Leu Lys Lys Glu Asp Leu
118 465          470          475          480
120 Val Asn Leu Glu Arg Met Gly Glu Lys Ser Ala Glu Asn Leu Leu Arg
121          485          490          495
123 Gln Ile Glu Glu Ser Lys Gly Arg Gly Leu Glu Arg Leu Leu Tyr Ala
124          500          505          510
126 Leu Gly Leu Pro Gly Val Gly Glu Val Leu Ala Arg Asn Leu Ala Leu
127          515          520          525
129 Arg Phe Gly His Met Asp Arg Leu Leu Glu Ala Gly Leu Glu Asp Leu
130          530          535          540
132 Leu Glu Val Glu Gly Val Gly Glu Leu Thr Ala Arg Ala Ile Leu Asn
133 545          550          555          560
135 Thr Leu Lys Asp Pro Glu Phe Arg Asp Leu Val Arg Arg Leu Lys Glu
136          565          570          575
138 Ala Gly Val Glu Met Glu Ala Lys Glu Arg Glu Gly Glu Ala Leu Lys
139          580          585          590

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141 Gly Leu Thr Phe Val Ile Thr Gly Glu Leu Ser Arg Pro Arg Glu Glu
142          595          600          605
144 Val Lys Ala Leu Leu Arg Arg Leu Gly Ala Lys Val Thr Asp Ser Val
145      610          615          620
147 Ser Arg Lys Thr Ser Phe Leu Val Val Gly Glu Asn Pro Gly Ser Lys
148 625          630          635          640
150 Leu Glu Lys Ala Arg Ala Leu Gly Val Pro Thr Leu Ser Glu Glu Glu
151          645          650          655
153 Leu Tyr Arg Leu Ile Glu Glu Arg Thr Gly Lys Asp Pro Arg Ala Leu
154      660          665          670
156 Thr Ala
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 2025
162 <212> TYPE: DNA
163 <213> ORGANISM: Thermus sp.
165 <400> SEQUENCE: 2
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167 aactacctct attacgtctt ggacgcccc gagatctccg acgccgagta cgaccggctc 120
168 cttaggggagc ttaaggagct ggaggagcgc ttccccgagc tcaaaagccc cgactcccc 180
169 acggaacagg tgggggagag gcctctggag gccaccttcc gcccgggtgcg ccacccccacc 240
170 cgcattgtact ccctggacaa cgccttttcc ttggacgagg tgaggggcctt tgaggagcgc 300
171 atagagcggg ccctggggcg gaaggggccc ttctctaca ccgtggagcg caaggtggac 360
172 ggtcttttccg tgaacctcta ctacgaggag ggcattctcg tctttggggc caccgggggc 420
173 gacgggggaga ccggggagga ggtgacctag aacctctcta ccatccccac cattccccgc 480
174 cgcctcacgg gcgttccgga ccgcctcgag gtccggggcg aggtctacat gccatagag 540
175 gccttctcta ggctcaacca ggagctggag gaggcggggg agcgcatctt caaaaacccc 600
176 aggaacgccc ccgcccgggc cttgcggcag aaagacccca gggtcacggc caggcggggc 660
177 ctgagggcca ctttttacgc cctggggctg ggcctggagg aaaccgggtt aaaaagccag 720
178 cacgaccttc tcctatggct aagagagcgg ggctttcccg tggagcacgg ctttaccgg 780
179 gccctggggg cggagggggt ggaggaggtc taccaggcct ggctcaagga gaggcggaag 840
180 cttccctttg aggccgacgg ggtggtggtc aagctggacg acctcgccct ctggcgggag 900
181 ctgggggtaca ccgcccgcac cccccgcttc gccctcgctt acaagttccc ggccgaggag 960
182 aaggagaccc gcctcctctc cgtggccttc cagggtggggc ggaccgggag catcaccccc 1020
183 gtgggcggtt tggagcccggt cttcatagag ggcagcgagg tgagccgggt caccctccac 1080
184 aacgagagct tcattgagga gctggacgtg cgcacggcg actgggtgct ggtccacaag 1140
185 gcgggagggg tgattcccgga ggtgctgagg gtccctgaaag agcgccgcac cggggaggag 1200
186 aagcccatca tctggcccga gaactgcccc gagtgcggcc acgcccctcat caaggagggg 1260
187 aaggtccacc gctgcccaca ccccttgtgc cccgccaagc gctttgaggc catccgccac 1320
188 tacgcctccc gcaaggccat ggacatccag ggctggggg agaagctcat agaaaagctt 1380
189 ctggaagagg gcctggtccg ggacgtggcc gacctctacc gcctgaagaa ggaggacctg 1440
190 gtgaacctgg agcgcatggg ggagaagagc gcagagaacc tcctccgcca gatagaggag 1500
191 agcaagggcc gcgccctgga gcgcctcctt tacgcctgg gccttcccg ggtgggggag 1560
192 gtgctggccc ggaacctggc cctccgcttc ggccacatgg accgccttct ggaggcgggc 1620
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195 atggaggcca aagagcggga gggcgaggcc ttgaaggggc tcaccttctg catcacggg 1800
196 gagctttccc ggccccggga ggaggtgaag gccctcctta ggcggttg ggccaagggtg 1860
197 acggactcgg tgagccgcaa gacgagcttc ctggtggtgg gggagaaccc ggggagcaag 1920
198 ctggaagagg ccgcgcctt gggggctccc acctgagcgg aggaggagct ctaccgcctc 1980

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```

199 attgaggaga ggacgggcaa ggacccaagg gccctcacgg cctag                2025
202 <210> SEQ ID NO: 3
203 <211> LENGTH: 20
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: Description of Artificial Sequence: probe or
209     primer
211 <220> FEATURE:
212 <221> NAME/KEY: tRNA
213 <222> LOCATION: (4)
214 <223> OTHER INFORMATION: w at position 4 can be T or A
216 <220> FEATURE:
217 <221> NAME/KEY: unsure
218 <222> LOCATION: (5)
219 <223> OTHER INFORMATION: s at position 5 can be C or G
221 <220> FEATURE:
222 <221> NAME/KEY: unsure
223 <222> LOCATION: (12)
224 <223> OTHER INFORMATION: s at position 12 can be C or G
226 <220> FEATURE:
227 <221> NAME/KEY: unsure
228 <222> LOCATION: (15)
229 <223> OTHER INFORMATION: r at position 15 can be G or A
231 <220> FEATURE:
232 <221> NAME/KEY: unsure
233 <222> LOCATION: (18)
234 <223> OTHER INFORMATION: y at position 18 can be T or C
236 <400> SEQUENCE: 3
237 atcwscgacg csgartayga                20
240 <210> SEQ ID NO: 4
241 <211> LENGTH: 7
242 <212> TYPE: PRT
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence: protein
248 <400> SEQUENCE: 4
249 Ile Ser Asp Ala Glu Tyr Asp
250     1             5
253 <210> SEQ ID NO: 5
254 <211> LENGTH: 20
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Description of Artificial Sequence: probe or
260     primer
262 <220> FEATURE:
263 <221> NAME/KEY: unsure
264 <222> LOCATION: (3)

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Input Set : A:\C26151.app

Output Set: N:\CRF4\09112003\I830502A.raw

265 <223> OTHER INFORMATION: s at position 3 can be C or G
 267 <220> FEATURE:
 268 <221> NAME/KEY: unsure
 269 <222> LOCATION: (6)
 270 <223> OTHER INFORMATION: s at position 6 can be C or G
 272 <220> FEATURE:
 273 <221> NAME/KEY: unsure
 274 <222> LOCATION: (8)
 275 <223> OTHER INFORMATION: k at position 8 can be G or T
 277 <220> FEATURE:
 278 <221> NAME/KEY: unsure
 279 <222> LOCATION: (9)
 280 <223> OTHER INFORMATION: s at position 9 can be G or C
 282 <220> FEATURE:
 283 <221> NAME/KEY: unsure
 284 <222> LOCATION: (12)
 285 <223> OTHER INFORMATION: s at position 12 can be G or C
 287 <220> FEATURE:
 288 <221> NAME/KEY: unsure
 289 <222> LOCATION: (15)
 290 <223> OTHER INFORMATION: y at position 15 can be C or T
 292 <220> FEATURE:
 293 <221> NAME/KEY: unsure
 294 <222> LOCATION: (18)
 295 <223> OTHER INFORMATION: r at position 18 can be A or G
 297 <400> SEQUENCE: 5
 298 ccsgtsccksc csacytgraa 20
 301 <210> SEQ ID NO: 6
 302 <211> LENGTH: 20
 303 <212> TYPE: DNA
 304 <213> ORGANISM: Artificial Sequence
 306 <220> FEATURE:
 307 <223> OTHER INFORMATION: Description of Artificial Sequence: probe or
 308 primer
 310 <220> FEATURE:
 311 <221> NAME/KEY: unsure
 312 <222> LOCATION: (9)
 313 <223> OTHER INFORMATION: v at position 9 can be C, G, or A
 315 <220> FEATURE:
 316 <221> NAME/KEY: unsure
 317 <222> LOCATION: (11)
 318 <223> OTHER INFORMATION: r at position 11 can be A or G
 320 <220> FEATURE:
 321 <221> NAME/KEY: unsure
 322 <222> LOCATION: (12)
 323 <223> OTHER INFORMATION: y at position 12 can be T or C
 325 <220> FEATURE:
 326 <221> NAME/KEY: unsure
 327 <222> LOCATION: (16)

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/830,502A

DATE: 09/11/2003
TIME: 10:33:47

Input Set : A:\C26151.2.app
Output Set: N:\CRF4\09112003\I830502A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:15; Xaa Pos. 37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55
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Seq#:15; Xaa Pos. 75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93
Seq#:15; Xaa Pos. 94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109
Seq#:15; Xaa Pos. 110,111,112,113,114,115,116,117,118,119,120,126,127,128
Seq#:15; Xaa Pos. 129,130,131,132,133,134,135,136,137,138,139,140,141,142
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Seq#:15; Xaa Pos. 157,158,159,160,161,162,163,164,165,166,167,168,169,170
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